The sequence at the junction of wsbellpro1 and GFP was:
(SEQ ID NO: 22)
5′ GCGACTGGCT GACTCAATCA CTACGCGGGG ATCCATGGTG AGCAAGGGCG 3′.

REMARKS

Applicants submit this Amendment to indicate the insertion point for the substitute Sequence Listing filed concurrently herewith. Applicants respectfully request examination on the merits of this application.

Receipt of the initial Office Action on the merits is awaited.

Respectfully submitted,

19 February 2002
Date

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Versions with Markings to Show Changes Made

IN THE SPECIFICATION

Please replace the paragraph beginning on page 29 at line 28 with the following rewritten paragraph:

Analysis of the promoter for *wSBE I-D4* allows us to investigate the presence of motifs previously described for promoters that regulate gene expression in the endosperm. Forde *et al* (1985) compared prolamin promoters, and suggested that the presence of a motif approximately -300 bp upstream of the transcription start point, called the endosperm box, was responsible for endosperm-specific expression. The endosperm box was subsequently considered to consist of two different motifs: the endosperm motif (EM) (canonical sequence TGTAAAG) and the GCN 4 motif (canonical sequence (SEQ ID NO: 18)G/ATGAG/CTCAT). The GCN4 box is considered to regulate expression according to nitrogen availability (Muller and Knudsen, 1993). The *wSBE I-D4* promoter contains a number of imperfect EM-like motifs at approximately -100, -300 and -400 as well as further upstream. However, no GCN4 motifs could be found, which lends support to the idea that this motif regulates response to nitrogen, as starch biosynthesis is not as directly dependent on the nitrogen status of the plant as storage protein synthesis. Comparison of the promoters for *wSBE I-D4* and *D2* (Rahman *et al*, 1997) indicates that although there are no extensive sequence homologies there is a region of about 100 bp immediately before the first encoded methionine where the homology is 61% between the two promoters. In particular there is an almost perfect match in the sequence over twenty base pairs (SEQ ID NO:19)CTCGTTGCTTCC/TACTCCACT, (positions 4723-4742 of the *wSBE I* sequence), but the significance of this is hard to gauge, as it does not occur in the rice promoter for SBE I. The availability of more promoters for starch biosynthetic enzymes may allow firmer conclusions to be drawn. There are putative CAAT and TATA motifs at positions 4870 and 4830 respectively of *wSBE I-D4* sequence. The putative start of translation of the mRNA is at position 4900 of *wSBE I-D4.*

Please replace the paragraphs beginning on page 45 at lines 15, 24, 29 and 33 with the following rewritten paragraphs, respectively:

(SEQ ID NO: 20)
5′ GCGGCCGCTC CCTGGCCGAC TTGGCCGAAG CTTGCATGCC TGCAGGTCGA CTCTAGAGGA TCCCCGGGTA CCGAGCTCGA ATTCATCGAT GATATCAGAT CCGGGCCCTC TAGATGCGGC CGCATGCATA AGCTT 3′

(SEQ ID NO: 21)
5′....CGCGCGCCCA CACCCTGCAG GTCGACTCTA GAGGATCCAT GGTGAGCAAG 3′.

The sequence at the junction of wsbellpro1 and GFP was:
(SEQ ID NO: 22)
5′ GCGACTGGCT GACTCAATCA CTACGCGGGG ATCCATGGTG AGCAAGGGCG 3′.